

# SEQUENCE LISTING

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<120> METHOD AND KIT FOR DETECTING A RISK OF DIABETES OR A METABOLIC SYNDROME

<130> 0933-0247PUS1

<140> US 10/538,198  
<141> 2005-06-09

<150> PCT/FI03/00946  
<151> 2003-12-11

<150> FI 20022178  
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<170> PatentIn version 3.1

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<212> DNA  
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<223> ADRA2B variant type sequence

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gcg gcc atc acc ttc ctc att ctc ttt acc atc ttc ggc aac gct ctg 96  
Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu  
20 25 30  
gtc atc ctg gct gtg ttg acc agc cgc tcg ctg cgc gcc cct cag aac 144  
Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn  
35 40 45  
ctg ttc ctg gtg tcg ctg gcc gcc gcc gac atc ctg gtg gcc acg ctc 192  
Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu  
50 55 60  
atc atc cct ttc tcg ctg gcc aac gag ctg ctg ggc tac tgg tac ttc 240  
Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe  
65 70 75 80  
cgg cgc acg tgg tgc gag gtg tac ctg gcg ctc gac gtg ctc ttc tgc 288  
Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys

85	90	95	
acc tcg tcc atc gtg cac. ctg tgc gcc atc agc ctg gac cgc tac tgg			336
Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp			
100	105	110	
gcc gtg agc cgc gcg ctg gag tac aac tcc aag cgc acc ccg cgc cgc			384
Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg			
115	120	125	
atc aag tgc atc atc ctc act gtg tgg ctc atc gcc gcc gtc atc tcg			432
Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser			
130	135	140	
ctg ccg ccc ctc atc tac aag ggc gac cag ggc ccc cag ccg cgc ggg			480
Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly			
145	150	155	160
cgc ccc cag tgc aag ctc aac cag gag gcc tgg tac atc ctg gcc tcc			528
Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser			
165	170	175	
agc atc gga tct ttc ttt gct cct tgc ctc atc atg atc ctt gtc tac			576
Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr			
180	185	190	
ctg cgc atc tac ctg atc gcc aaa cgc agc aac cgc aga ggt ccc agg			624
Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg			
195	200	205	
gcc aag ggg ggg cct ggg cag ggt gag tcc aag cag ccc cga ccc gac			672
Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp			
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cat ggt ggg gct ttg gcc tca gcc aaa ctg cca gcc ctg gcc tct gtg			720
His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val			
225	230	235	240
gct tct gcc aga gag gtc aac gga cac tcg aag tcc act ggg gag aag			768
Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys			
245	250	255	
gag gag ggg gag acc cct gaa gat act ggg acc cgg gcc ttg cca ccc			816
Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro			
260	265	270	
agt tgg gct gcc ctt ccc aac tca ggc cag ggc cag aag gag ggt gtt			864
Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val			
275	280	285	
tgt ggg gca tct cca gag gat gaa gct gaa gag gag gaa gag gag gag			912
Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Glu			
290	295	300	
gag gag tgt gaa ccc cag gca gtg cca gtg tct ccg gcc tca gct tgc			960
Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala Ser Ala Cys			
305	310	315	320

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 Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu Ala Thr Leu  
 325 330 335  
 cgt ggc cag gtg ctc ctg ggc agg ggc gtg ggt gct ata ggt ggg cag 1056  
 Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile Gly Gly Gln  
 340 345 350  
 tgg tgg cgt cga agg gcg cac gtg acc cgg gag aag cgc ttc acc ttc 1104  
 Trp Trp Arg Arg Ala His Val Thr Arg Glu Lys Arg Phe Thr Phe  
 355 360 365  
 gtg ctg gct gtg gtc att ggc gtt ttt gtg ctc tgc tgg ttc ccc ttc 1152  
 Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp Phe Pro Phe  
 370 375 380  
 ttc ttc agc tac agc ctg ggc gcc atc tgc ccg aag cac tgc aag gtg 1200  
 Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His Cys Lys Val  
 385 390 395 400  
 ccc cat ggc ctc ttc cag ttc ttc ttc tgg atc ggc tac tgc aac agc 1248  
 Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr Cys Asn Ser  
 405 410 415  
 tca ctg aac cct gtt atc tac acc atc ttc aac cag gac ttc cgc cgt 1296  
 Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp Phe Arg Arg  
 420 425 430  
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 35 40 45  
 Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu  
 50 55 60

Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe  
 65 70 75 80

Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys  
 85 90 95

Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp  
 100 105 110

Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg  
 115 120 125

Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser  
 130 135 140

Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly  
 145 150 155 160

Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser  
 165 170 175

Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr  
 180 185 190

Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg  
 195 200 205

Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp  
 210 215 220

His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val  
 225 230 235 240

Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys  
 245 250 255

Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro  
 260 265 270

Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val  
 275 280 285

Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu

290                      295                      300  
 Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala Ser Ala Cys  
 305                      310                      315                      320  
 Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu Ala Thr Leu  
                     325                      330                      335  
 Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile Gly Gly Gln  
                     340                      345                      350  
 Trp Trp Arg Arg Arg Ala His Val Thr Arg Glu Lys Arg Phe Thr Phe  
                     355                      360                      365  
 Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp Phe Pro Phe  
                     370                      375                      380  
 Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His Cys Lys Val  
 385                      390                      395                      400  
 Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr Cys Asn Ser  
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 Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp Phe Arg Arg  
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 gcg gcc atc acc ttc ctc att ctc ttt acc atc ttc ggc aac gct ctg                      96  
 Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu  
                     20                      25                      30

gtc atc ctg gct gtg ttg acc agc cgc tcg ctg cgc gcc cct cag aac Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn 35 40 45	144
ctg ttc ctg gtg tgc ctg gcc gcc gcc gac atc ctg gtg gcc acg ctc Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu 50 55 60	192
atc atc cct ttc tgc ctg gcc aac gag ctg ctg ggc tac tgg tac ttc Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe 65 70 75 80	240
cgg cgc acg tgg tgc gag gtg tac ctg gcg ctc gac gtg ctc ttc tgc Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys 85 90 95	288
acc tcg tcc atc gtg cac ctg tgc gcc atc agc ctg gac cgc tac tgg Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp 100 105 110	336
gcc gtg agc cgc gcg ctg gag tac aac tcc aag cgc acc ccg cgc cgc Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg 115 120 125	384
atc aag tgc atc atc ctc act gtg tgg ctc atc gcc gcc gtc atc tcg Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser 130 135 140	432
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cgc ccc cag tgc aag ctc aac cag gag gcc tgg tac atc ctg gcc tcc Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser 165 170 175	528
agc atc gga tct ttc ttt gct cct tgc ctc atc atg atc ctt gtc tac Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr 180 185 190	576
ctg cgc atc tac ctg atc gcc aaa cgc agc aac cgc aga ggt ccc agg Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg 195 200 205	624
gcc aag ggg ggg cct ggg cag ggt gag tcc aag cag ccc cga ccc gac Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp 210 215 220	672
cat ggt ggg gct ttg gcc tca gcc aaa ctg cca gcc ctg gcc tct gtg His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val 225 230 235 240	720
gct tct gcc aga gag gtc aac gga cac tcg aag tcc act ggg gag aag Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys 245 250 255	768

gag gag ggg gag acc cct gaa gat act ggg acc cgg gcc ttg cca ccc Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro 260 265 270	816
agt tgg gct gcc ctt ccc aac tca ggc cag ggc cag aag gag ggt gtt Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val 275 280 285	864
tgt ggg gca tct cca gag gat gaa gct gaa gag gag gaa gag gag gag Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Glu 290 295 300	912
gag gag gag gaa gag tgt gaa ccc cag gca gtg cca gtg tct ccg gcc Glu Glu Glu Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala 305 310 315 320	960
tca gct tgc agc ccc ccg ctg cag cag cca cag ggc tcc cgg gtg ctg Ser Ala Cys Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu 325 330 335	1008
gcc acc cta cgt ggc cag gtg ctc ctg ggc agg ggc gtg ggt gct ata Ala Thr Leu Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile 340 345 350	1056
ggg ggg cag tgg tgg cgt cga agg gcg cac gtg acc cgg gag aag cgc Gly Gly Gln Trp Trp Arg Arg Ala His Val Thr Arg Glu Lys Arg 355 360 365	1104
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ttc cgc cgt gcc ttc cgg agg atc ctg tgc cgc ccg tgg acc cag acg Phe Arg Arg Ala Phe Arg Arg Ile Leu Cys Arg Pro Trp Thr Gln Thr 435 440 445	1344
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Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn  
35 40 45

Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu  
50 55 60

Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe  
65 70 75 80

Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys  
85 90 95

Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp  
100 105 110

Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg  
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Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser  
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Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly  
145 150 155 160

Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser  
165 170 175

Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr  
180 185 190

Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg  
195 200 205

Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp  
210 215 220



His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val  
 225 230 235 240

Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys  
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Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro  
 260 265 270

Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val  
 275 280 285

Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu  
 290 295 300

Glu Glu Glu Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala  
 305 310 315 320

Ser Ala Cys Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu  
 325 330 335

Ala Thr Leu Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile  
 340 345 350

Gly Gly Gln Trp Trp Arg Arg Arg Ala His Val Thr Arg Glu Lys Arg  
 355 360 365

Phe Thr Phe Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp  
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Phe Pro Phe Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His  
 385 390 395 400

Cys Lys Val Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr  
 405 410 415

Cys Asn Ser Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp  
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Ala Trp  
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